

STEVEN M. FOLTZ

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EDUCATION

PhD, Washington University in St. Louis, St. Louis, MO June 2014 – present
Division of Biology and Biomedical Sciences Expected defense: Fall 2019
Human and Statistical Genetics Program
Precision Medicine Pathway
Advisor: Li Ding, PhD
Thesis: Multi-platform genomics and transcriptomics integration for gene fusion discovery and somatic mutation haplotyping in cancer

MS, University of Washington, Seattle, WA September 2011 – August 2013
Biostatistics
Advisors: Brian Browning, PhD, and Sharon Browning, PhD
Thesis: Rare variant method for identity-by-descent detection in sequence data, and the time to most recent common ancestor given identity-by-descent segment length

BS, Presbyterian College, Clinton, SC August 2006 – April 2010
Mathematics, *summa cum laude*
Advisor: Doug Daniel, PhD
Thesis:

RESEARCH EXPERIENCE

Washington University in St. Louis, St. Louis, MO June 2014 – present
Graduate student, Laboratory of Li Ding, PhD
Thesis: Multi-platform genomics and transcriptomics integration for gene fusion discovery and somatic mutation haplotyping in cancer

- Pan-cancer computational projects utilizing tumor and normal tissue sequencing data (DNA, RNA, methylation) to understand multiple types of germline and somatic variation
- Large-scale data analysis tool and pipeline development
- Bulk, single cell, and linked-read sequencing data analysis
- Gene fusion discovery in 9,000+ patients from The Cancer Genome Atlas and a large multiple myeloma cohort

- Linked-read sequencing data analysis for phasing somatic variation and modeling tumor evolution

This work has led to 2 published first author papers in *Bioinformatics* and *Cell Reports*, 2 more under review, and 4 co-author papers in *Cell*, *Nature Medicine*, *Molecular Psychiatry*, and *Annals of Oncology*.

Virginia Commonwealth University, Richmond, VA

August 2013 – May 2014

Biostatistician, Laboratory of Nengliang Yao, PhD

- Led statistical aspects of cancer care research as part of a health policy team
- Procured, cleaned, and analyzed data from national cancer databases, including SEER
- Developed geographically weighted regression and spatial panel data models

This work led to a co-author publication in *PLoS ONE*.

University of Washington, Seattle, WA

September 2011 – August 2013

Research assistant, Laboratory of Brian Browning, PhD, and Sharon Browning, PhD

Thesis: Rare variant method for identity-by-descent detection in sequence data, and the time to most recent common ancestor given identity-by-descent segment length

- Implemented novel algorithms to define identity-by-descent (IBD) between individuals using rare DNA variation
- Worked with data from the 1000 Genomes Project and simulated coalescent model data
- Assisted in methods development for missing data imputation, haplotype phasing, and IBD detection

Presbyterian College, Clinton, SC

Spring 2010

Honors research in mathematics, advised by Doug Daniel, PhD

Developed analytical and computational approaches to answer an open question about tiling deficient rectangular fields with trominos.

Medical University of South Carolina, Charleston, SC

Summer 2009

Summer Research Fellow, Laboratory of Jim Zheng, PhD

Created a weighted clustering coefficient to detect regions of high interconnectivity in yeast gene networks based on synthetic lethal interactions.

Presbyterian College, Clinton, SC

Fall 2008 – Spring 2009

Research assistant, Laboratory of James Wanliss, PhD

Analyzed space weather data as part of a programming team to refine solar storm prediction models.

RESEARCH GRANTS

Paula C. and Rodger O. Riney Blood Cancer Research Initiative Fund

Washington University School of Medicine

Funding since Fall 2017: \$25 million

PIs include: Li Ding, PhD

My contributions:

- Multiple myeloma gene fusion discovery project
- Single cell RNA-seq analysis
- Preparation and delivery of multiple donor presentations

HONORS AND AWARDS

- “Best of *Cell Reports* 2018” for co-first author publication titled “Driver Fusions and Their Implications in the Development and Treatment of Human Cancers.”
- “Outstanding Mentor”, recognizing one mentor working with high schoolers from St. Louis through the Washington University Young Scientist Program (25th Anniversary Gala, October 22, 2016).

PUBLICATIONS

1. Sanchez-Vega, F., M. Mina, J. Armenia, W. K. Chatila, A. Luna, K. C. La, S. Dimitriadou, D. L. Liu, H. S. Kantheti, S. Saghafeinia, D. Chakravarty, F. Daian, Q. Gao, M. H. Bailey, W. W. Liang, **S. M. Foltz**, I. Shmulevich, L. Ding, Z. Heins, A. Ochoa, B. Gross, J. Gao, H. Zhang, R. Kundra, C. Kandoth, I. Bahceci, L. Dervishi, U. Dogrusoz, W. Zhou, H. Shen, P. W. Laird, G. P. Way, C. S. Greene, H. Liang, Y. Xiao, C. Wang, A. Iavarone, A. H. Berger, T. G. Bivona, A. J. Lazar, G. D. Hammer, T. Giordano, L. N. Kwong, G. McArthur, C. Huang, A. D. Tward, M. J. Frederick, F. McCormick, M. Meyerson, N. Cancer Genome Atlas Research, E. M. Van Allen, A. D. Cherniack, G. Ciriello, C. Sander and N. Schultz (2018). “Oncogenic Signaling Pathways in The Cancer Genome Atlas.” *Cell* **173**(2): 321-337 e310.
2. Gao, Q.*, W. W. Liang*, **S. M. Foltz***, G. Mutharasu, R. G. Jayasinghe, S. Cao, W. W. Liao, S. M. Reynolds, M. A. Wyczalkowski, L. Yao, L. Yu, S. Q. Sun, G. Fusion Analysis Working, N. Cancer Genome Atlas Research, K. Chen, A. J. Lazar, R. C. Fields, M. C. Wendl, B. A. Van Tine, R. Vij, F. Chen, M. Nykter, I. Shmulevich and L. Ding (2018). “Driver Fusions and Their Implications in the Development and Treatment of Human Cancers.” *Cell Rep* **23**(1): 227-238 e223. *Co-first authors contributed equally.
3. Dang, H. X., B. S. White, **S. M. Foltz**, C. A. Miller, J. Luo, R. C. Fields and C. A. Maher (2017). “ClonEvol: clonal ordering and visualization in cancer sequencing.” *Ann Oncol* **28**(12): 3076-3082.
4. **Foltz, S. M.**, W. W. Liang, M. Xie and L. Ding (2017). “MIRMMR: binary classification of microsatellite instability using methylation and mutations.” *Bioinformatics* **33**(23): 3799-3801.

5. Olfson, E., N. L. Saccone, E. O. Johnson, L. S. Chen, R. Culverhouse, K. Doheny, **S. M. Foltz**, L. Fox, S. M. Gogarten, S. Hartz, K. Hetrick, C. C. Laurie, B. Marosy, N. Amin, D. Arnett, R. G. Barr, T. M. Bartz, S. Bertelsen, I. B. Borecki, M. R. Brown, D. I. Chasman, C. M. van Duijn, M. F. Feitosa, E. R. Fox, N. Franceschini, O. H. Franco, M. L. Grove, X. Guo, A. Hofman, S. L. Kardina, A. C. Morrison, S. K. Musani, B. M. Psaty, D. C. Rao, A. P. Reiner, K. Rice, P. M. Ridker, L. M. Rose, U. M. Schick, K. Schwander, A. G. Uitterlinden, D. Vojinovic, J. C. Wang, E. B. Ware, G. Wilson, J. Yao, W. Zhao, N. Breslau, D. Hatsukami, J. A. Stitzel, J. Rice, A. Goate and L. J. Bierut (2016). "Rare, low frequency and common coding variants in CHRNA5 and their contribution to nicotine dependence in European and African Americans." *Mol Psychiatry* **21**(5): 601-607.
6. Ye, K., J. Wang, R. Jayasinghe, E. W. Lameijer, J. F. McMichael, J. Ning, M. D. McLellan, M. Xie, S. Cao, V. Yellapantula, K. L. Huang, A. Scott, **S. Foltz**, B. Niu, K. J. Johnson, M. Moed, P. E. Slagboom, F. Chen, M. C. Wendl and L. Ding (2016). "Systematic discovery of complex insertions and deletions in human cancers." *Nat Med* **22**(1): 97-104.
7. Yao, N., **S. M. Foltz**, A. Y. Odisho and D. C. Wheeler (2015). "Geographic analysis of urologist density and prostate cancer mortality in the United States." *PLoS One* **10**(6): e0131578.

TEACHING EXPERIENCE

Washington University in St. Louis, St. Louis, MO

Instructor, Introduction to Python – Bioinformatics Winter 2019

Student profile: 6 post-baccalaureate students from the Opportunities in Genomics Research diversity outreach program.

Responsibilities: Developed syllabus, created course content, led weekly classroom lectures and activities, gathered regular feedback.

Teaching assistant, Genomics (Biol 5488) Spring 2016

Student profile: 40 first-year graduate students with different academic backgrounds and programming skills.

Responsibilities: Taught scientific and computational concepts for weekly genomics programming labs (Python), hosted office hours, evaluated student performance on labs and exams (one of four TAs).

Tutor, Fundamentals of Biostatistics for Graduate Students (Biol 5075) Fall 2015, Fall 2016

Student profile: 30 first-year graduate students with varying skill levels.

Responsibilities: Taught background genomics and computer coding skills (Python) for programming lab assignments.

Presbyterian College, Clinton, SC

Tutor, Department of Mathematics January 2007 – April 2010

Student profile: Individuals or groups of students from courses up to Calculus II. Responsibilities: Taught core concepts underlying problem sets to help students understand their homework.

MENTORING EXPERIENCE

Mentoring for Ding Lab rotation graduate students

- Yize Li
Fall 2017
Current status: joined the lab
- Ruiyang Liu
Fall 2017
Current status: joined the lab
- Lijun Yao
Fall 2017
Current status: joined the lab

Mentoring for Ding Lab undergraduate students

- Moses Schindler
Summer – Fall 2019
Current status: WashU, Class of 2023
- Jessika Baral
Fall 2018
Current status: WashU, Class of 2021
- Guanlan Dong
Fall 2018, Spring 2019
Graduated WashU: Spring 2019
Current status: graduate student at Harvard University
- Justin Chen
Summer 2018
Current status: Columbia University, Class of 2022
- Edwin Qiu
Spring 2018, Fall 2018
Current status: WashU, Class of 2020

Mentoring for the Washington University Young Scientist Program

- Jada Reid

Fall 2014 – Spring 2018

Graduated Collegiate School of Medicine and Bioscience: Spring 2018

Current status: Wesleyan University , Class of 2022

SERVICE AND OUTREACH

Washington University Young Scientist Program, St. Louis, MO

Leader of Mentoring Program Cohort

Fall 2014 – Spring 2018

- Led 12 graduate students paired with high schoolers for four years
- Coordinated bi-weekly school visits and field trips
- Mentored one student (Jada Reid, Wesleyan University 2022)

St. Louis Science Center, St. Louis, MO

Exhibit interpreter

Summer 2015

- Smithsonian and NHGRI funded Genome: Unlocking Life's Code
 - Discussed the science, ethics, and societal impacts of genomics with museum patrons
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PRESENTATIONS

Oral presentations

- “” WashU DBBS Precision Medicine Pathway Retreat. Spring 2016.
- “” WashU DBBS Precision Medicine Pathway Retreat. Spring 2017.

Poster presentations

- “” International Myeloma Workshop. Boston, MA. September 2019.
- “” American Society of Hematology. San Diego, CA. December 2018.
- “” WashU DBBS Human and Statistical Genetics Program Retreat. Potosi, MO. September 2017.
- “Genomic region and sample selection strategy for variant discovery and association analysis”. Genome Informatics. Cold Spring Harbor, NY. October, 2015.

- “Comprehensive Analysis of Germline Complex Insertions and Deletions”. WashU DBBS Molecular Genetics and Genomics / Computational and Systems Biology Joint Program Retreat. New Haven, MO. September, 2015.
- “Comprehensive Analysis of Germline Complex Insertions and Deletions”. WashU DBBS Human and Statistical Genetics Program Retreat. St. Louis, MO. September, 2015.
- “Identity-by-descent analysis of sequence data”. International Genetic Epidemiology Society. Stevenson, WA. October 2012.

OTHER WORK EXPERIENCE

Across, Nairobi, Kenya

September 2010 – July 2011

Institutional and Organizational Development Volunteer

Promoted the organization and its mission (holistic transformation of South Sudan communities) to an international audience through the website and other publications. Placement coordinated through the Presbyterian Church (U.S.A.) Young Adult Volunteers program.

RESEARCH SKILLS

- Programming languages: R, Python, Bash, Unix command line (github.com/envest)
- Bioinformatics tools: fusion detection, 10x Long Ranger, GATK, samtools, bedtools, Integrated Genomics Viewer (IGV)
- Data presentation tools: ggplot2 (R package), Adobe Illustrator, L^AT_EX
- Analysis of large scale sequencing data (DNA, RNA) and file formats (VCF, BAM, MAF, BED) on large Unix clusters
- Multi-institutional collaboration on projects, e.g. The Cancer Genome Atlas (TCGA), Clinical Proteomic Tumor Analysis Consortium (CPTAC), Multiple Myeloma Research Foundation (MMRF)

GRADUATE SCHOOL COURSEWORK

Washington University in St. Louis, St. Louis, MO

June 2014 – present

Ph.D. Human and Statistical Genetics (GPA: 4.00/4.00)

Human Linkage and Association Analysis; Fundamentals of Mammalian Genetics; Computational Statistical Genetics; Genomics; Human Genetics Journal Club; Precision Medicine Pathway; Ethics and Research Science

University of Washington, Seattle, WA

September 2011 – August 2013

MS Biostatistics (GPA: 3.43/4.00)

Biostatistics I, II; Statistical Inference I, II; Theory of Linear Models; Statistical Genetics I; Categorical Data Analysis; Survival Data Analysis; Evolutionary Genetics; Population Genetics; Statistical Genetics Seminar; Biostatistics Seminar

The Teaching Center

September 2015 – present

Teaching Citation (three semester-long teaching experiences)

WU-CIRTL program for future STEM faculty (associate level)

Young Scientist Program mentor

September 2014 – May 2018

Mentored high school students in program designed to promote interest in science and medicine.

PROFESSIONAL DEVELOPMENT

- Teaching Center
- SEPAL Active Learning seminar
- Mentor training
- Early Career Workshop
- Science Communication class

Last updated: September 3, 2019